



Matches	277: Conservative	86: Mismatches	228: Indels	12: Gaps
QY	22 PARLG-LPLRLRLLLMAAASAOCHLSGRPIFAWKGHVGQDRVDFGQEPHTVLEH	80		
Db	45 PAAMGFLCVISRLIMLT-SAITAASKRFIDKRELLLVNLTDGCGHNF-FGPOEPHTVLEH	102		
QY	81 EGGSSVWVGKGGKYULPREFREGKASVATVINGSKGSCLDKROCEVITLLERSSETL	140		
Db	103 SLNSSVVYVGGNNITYLEFEFAHSSNASTALINTSTHNTHRLSTCEINTLLHMOITDL	162		
QY	141 LACGTNARHPSCMNLVNGTVLPGEMRGYAPSPSPDENSLYLEGDEGVSTTIKROENKTI	200		
Db	163 LACGTNSQKPSRCOMLNLNLTQFLGPRGLGAPSPSSGNLYLEFDQNDYSTITLYKSLSS	222		
QY	201 PRRRIRGESELYTSDTYQMNQPFQIKATIVHODQAYDKIYFFREDNDPKNEAPLANS	260		
Db	223 HKFRIRAGVVELYTSPTAHNRQFQVQATVHNKNESSYDDKIYFFQENSHSDPKFRPHTPV	282		
QY	261 RAAOLCRGGGGESSLSYSKANTPLKAMVCSDAATNKNFNLQVETLLRDPSSGQMDRTR	320		
Db	283 RGVQVCSDDGGESSLSYKMTPLKARLACVADYDGTGRVNLQDIFLWQAPENSMETTL	342		
QY	321 YVGVSPNPNYAVCVSYSLGDIIDKVFRTSSLYGHSSLPNPRGKCLPDDQPIPTREFOY	380		
Db	343 IYGLFLSPNPNFSAVCVFYTKYDIDNHFKTSKLNKYNHKKLPTRRPGCKMKNQNVPRETQY	402		
QY	381 ADNRPEVAORVERPWRGLKPLTFHSHKYHYOKAVNHRMQASHGETF--HYLYLTFTDGTIHK	438		
Db	403 ADREYVEADPRVYQKNNAMPRIQSKYIYTKLLVRYVE--YGVGFVAFTIYLTITIKGTIHI	460		
QY	439 VVEPREGHSFAFNIMETOPRRRAALIQMSLDAERKKIYSSQWHEVSYVRLDLEVGG	498		
Db	461 YVREDNSNTALNLTLEINPFQKPAPIQNIILDNLTNKLKYNSEWSEVSPRLDLSYGN	520		
QY	499 CGHGELSHDPICGMDQGRICISYSEKSYLOSINPAEP--HKECPPNPKDAPLQKYSL	556		
Db	521 DCFSCFMSDRPLCTYNYNNC---SFKQRKSVETGGRANTTSEMGCDHAPRVVAKHYSI	577		
QY	557 ADRNSRYLSCPMESNRHATYSWRHKEVNEQSCERGHQSPNCILFIENLTAQOYGHYFCEAQ	616		
Db	578 PLLSSYLSLCPASVNSHADYFWTKDGFTEKRCYHVKTHKNDICILLIANSYTAGTNGTVCMNK	637		
QY	617 EGS 619			
Db	638 EDS 640			

[illegible]

RT	The complete sequences of 100 new cDNA clones from brain which code		
for	large proteins in vitro."		
BL	DNA Res. 7:347-355(2000).		
DR	EMBL, AB051532; BAB21336.1; -		
DR	InterPro: IPR003659; Plexin-like.		
DR	InterPro: IPR002165; Plexin_repeats.		
DR	InterPro: IPR001627; Sema.		
DR	Pfam: PF01437; PSI: 1.		
DR	Pfam: PF01403; Sema: 1.		
DR	SMART: SM00423; PSI: 1.		
FT	NON_TPR	1	
SO	SEQUENCE	893 AA; 98361 MW; D6C6C48DE52AF14 CRC64;	

Query Match	18.8%	Score	680.5	DB 4	Length	893;			
Best Local Similarity	30.1%	Pred.	No. 9.8e-49;						
Matches	220;	Conservative	89;	Mismatches	293;	Indels	129;	Gaps	29

[illegible]

RESULT 4	
Q8TB71	
ID	Q8TB71
PRELIMINARY;	PRT;
	748 AA.

AC O9NBZ1.  
DT 01-JUN-2002 (TReMBLrel. 21, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Hypothetical 83.0 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP  
RP SEQUENCE FROM N.A.  
RC  
RC TISSUE=MUSCLE;  
RA Strassberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC024220; AA02420.1; -.  
KW Hypothetical protein  
SQ SEQUENCE 748 AA; 85034 MW; 587C53CB65A84656 CRC64;

Query Match	17.1%	Score 617.5	DB 4	Length 748
Best Local Similarity	28.2%	Pred. No. 1.7e-43		
Matches 202; Conservative	92	Mismatches 293	Indels 129	Gaps 27

0Y	7	GAASAPARAPARPARGLRLRLRLLLMA----	AAASAGHLRSPRLFAVWKHV	62
0Y	11	GAASAPARAPARPARGLRLRLRLLLMA----	AAASAGHLRSPRLFAVWKHV	62
Db	2	GRAGAAAV---IPG-----	LALLMAVGLGSAAPSPRRLRLSPQELQAMH----	42
0Y	63	GODRVDGQTEPHVLYLHEPGSSVWVGGRGVYLFDP	PEGKNASVRYNI-----	111
Db	43	GIOTFSLERTCCYQALLVDEBGRILFVAGENNHASLNT---	DNISRAKKLAMPAPVEMR	99
0Y	114	-----GTRKSGCLDKRCDENYITLLERASE--	GLACGNNARIPSCWMLVNGVPLG--	16
Db	100	EBRCNAGKDIGT-----	ECMNFVKLLHAAYNRHLLACGSAEPIC-----	AEVEVGR 14
0Y	165	-----	EMRGAPSPDENSLVLEEGDEVSTIRKOEYNGKIP	PRFRIRGES 21
Db	149	AEPVRLRDPGRLEQKSGSPYDRPRRAASVLYG	ELYSVGAVALMGROFTIFRSLGQPR	20
0Y	211	ELYT---SPTWQNPQFKA-TIVHODAYDKITY	FFREDNDPKPE--APLNVSAVOL	26
Db	209	SLRTEPHDSRMNLNEPRFVFWFMIPESENDDKIX	IFFEFETAVEAPALGRLSVHVGQI	26
0Y	266	CRGDGQGESLSVSKMNTFLKAMLYOS--	DAATNKNFNLQOVFLLPDSGQWROTRVYG	32
Db	269	CRNDVGQGSRL--VNKHTTLKARLYCSV	GVESGDTHFDQLODYFL--SSRDRHTFLYA	32
0Y	324	VFSNP--WNYSACVYSLGDDIKVF-----	RTSSLKGHYSSLPNRPCKC-----	36
Db	326	VESTSIFEGSAAVCYSMNDVRAAFGLSPRANK	EGRMHOMVSYQRYVPRPGCPSKTEG	38
0Y	367	-LPDOQPIETEPFOVADRRPEVAORREPRGLKTP	FE--HSKYHOKAIVHOMOSHEE	42
Db	386	TFSSTKDFPDVYIOPARNHPLMYSVLPFG--	GRPLFLQVGAITYTTQTLAADRYAANDGH	44
0Y	423	TEHVLYLTTRDGTINHV--VEBGEDEHSEAF	NIMEIQPREAAIOTMSLDAERRKLVS	48
Db	444	-YDVLFEIGDVTYLVKVISVPGKSPSAGLLLE	ELHVEPDESAAYVSMQISSRHQLYYA	50
0Y	481	SQMEVYSQVPLDLCVYGGGCHCLMSRDYPC	MDQGRCLSIYSS--ERSVLDSINAEVA	53
Db	503	SSSAVAQIALHRCAAHGRCTECCLADRDYCA	MDGVAICRFQOPSAKRFRRRQVYRGDPS	56
0Y	539	KCPNPDKPRKAPLO--KVSILAPNSRYLSC	PMESRHATYSMRH-----	KEVNE 58
Db	563	TLCSSGSSRPALLLEHKHVEVEBSSAFLE	CEPRSLQARVEMTQORAGVTANHTQVLAEEKE	62
0Y	585	QSCPEGHOSPNCILTEINLTAAQYGHYFCEA	ODGSTRFQAQHWOLLPEDGIMAEHL	64
Db	623	RRARG-----	LLRLRRRDSGVYLCAAAVEQGTQPLRLSLHVSATQAE	RL 670

RESULT 5  
Q8TDV7

ID Q8TDV7 PRELIMINARY; PRT: 754 AA.  
 AC Q8TDV7;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Semaphorin 3B.  
 GN SEMA 3B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEMAPHORIN 3B (SEMA3B) CDNA."  
 RA Koyama N.;  
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB083186; BAB88870.1; -  
 SO SEQUENCE 754 AA; 83691 MW; E61FD08C04E9A68E CRC64;

Query Match 16.6%; Score 601.5; DB 4; Length 754;  
 Best Local Similarity 27.8%; Pred. No. 3.8e-42;  
 Matches 201; Conservative 93; Mismatches 293; Indels 135; Gaps 28;

7 GRAPAPRARRVPPRRRLGLRLRLLLLA-----AASAGHLRSGPRIFAVKCHV 62  
 2 GRAGAAV---TPG-----LALLMAVGLGSAAPSPPRLRSTFELQAMH--- 42  
 63 GQDVRDGEPTHTVLFHEPGSSVWVGNGKYLFDPECKNASVTVNT----- 113  
 43 GLQFSLERTCCYQALLVDEGRGLFVGAENHVASLNL---DNISKRKKLAMPARYEMR 99  
 114 -----GSKGCLDKDCENTITLERRSE-GLLAGCTNARHPSCMNLVNGTVPLG-- 164  
 100 EECMAKDKDGT-----ECMNFVLLAHAYRTHLLACGTGAFHPTC-----AEVEGHR 148  
 165 -----EMGYAFSPDENSLVLFEGDEVYSTRKQEVNGKIRPRFRIGES 210  
 149 AEEVVLALDPERIDGKSPYDPRHRAAYLVGEELYSGLAADMGRDFTIFNSLQGP 208  
 211 ELYT---SDTVMNPQFIKA-TIVHODQAVDKEYFEFREDNPKNE-AELNYSRYAQL 265  
 209 SLRTEPHDSRLNPEKFEVYFWIPESENPDODKIYFFRETAVEAAPALGLSTVSRVQOI 268  
 266 CRGQGGESSLSVSKMNTFLKAMLYCS--DAATKNKFRNL-----QVYLLPDSGGWRD 318  
 269 CRNVGGQORSL-VNKKWTFELKARLVCSVPVEGDTHPDLPPRAEDVFL--SSRDHRT 325  
 319 TRYGVGSPNP---KNYSAVCYVSLGIDIKVF-----RTSLKGYHSLPMPRGKC 366  
 326 PLIYAVSTSSITFGSAVCYVSMNDYRAFLGFAHKEGFMHGVSTIGKRVTPRGMC 385  
 367 -----LPDQPIPTETFOVADNRHPEVAORFERMGLKTPLF--HSKYHYQKVAHYRM 416  
 386 PSKTFGFEFSSTKDPRDDVIOGFARHNPMLYNSVLPTG--GRPLFLQVANGVYFTQIADRV 443  
 417 QASNGEFHYLYLTDTGTHIKV--VEEGEOHSAFANIMEIOFRRRAAIQYMSLDAER 474  
 444 AADAGH-YDVLEICTDGTDLKLVSVKGRSPAEGLLLELHVEDLSAATVSMQISSRK 502  
 475 RKLVSSOWEVSQVPLDCEYVGGGCHGLMSRPYCGMDGRCISYSS--ERSVLOSII 532  
 503 HOLYVASRAVAQIALHRCANAGHYCTECCILARPYCAMDVACTROPSPAKRRFRDDV 562  
 533 NPAPHECPNPKPKAPLQ-KVSLAPNSRYLLSCPMESRHATYSWRH----- 579  
 563 RNDGPRSLGSDSSRPALLHKKVFGVESSAFLECEPRSLDARVEMFQORGATYAHQYVL 622  
 580 -KENVEDSCERGHOSPNCILFIENLTAQOYGHYCEAOEGSYFREAOHWOLLDPDGIMAE 638  
 623 AAEERTERTARG-----LLRLRLRRDSGVLYCAVEGFTQPLRLSLHVLASATQAE 674  
 639 HL 640

Db 675 RL 676

RESULT 6  
 Q8GCU9 PRELIMINARY; PRT: 756 AA.  
 AC Q8GCU9;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Semaphorin 3F.  
 GN SEMA3F.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEMAPHORIN 3F (SEMA3F) CDNA."  
 RA Watanabe Y., Nakamura H.;  
 RT "Axon guidance of the trochlear nerve by Sema 3F along mid-hindbrain boundary."  
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB072930; BAB88691.1; -  
 SO SEQUENCE 756 AA; 85196 MW; C36754C02541EDB8 CRC64;

Query Match 16.5%; Score 597; DB 13; Length 756;  
 Best Local Similarity 28.7%; Pred. No. 9.3e-42;  
 Matches 202; Conservative 112; Mismatches 285; Indels 106; Gaps 33;

33 LLLLMMAAASAGHLNSGPRIFAVKCHVQGDVDC-----QTEPHTVLFHEPGSSVW 88  
 12 LLLTGMRAAHKDD-VPPTPRVQLSFELKATGAHFNFLNLSDDRIKLKDDHDMY 70  
 89 VGGKGYLVFDPECKN-----ASVRYVN--IGSKGCLDKDCENTITLLE--RR 136  
 71 VGSNDYVSLDLHINRPLLIHWPASQRIECLLSKNS--NGEGNFIIRLLQPMNR 127  
 137 SEGLLAGCTNARHPSCMNLVNGTVV-----PLGEMRYAFSPDENSLVLFEGDE 186  
 128 TH-LYVCGTAGVNPICAFINGRKAQDIYFLEPDKLESGKSYDKVDTVSLNIEE 186  
 187 VYSTIRKQEVNGKIPRRFRIGSEELITSPTV---MNPQFIKATV-HODQAVDKEY 241  
 187 LYAGV-YIDEMGTAAIFRTGKOTAMRTDQYNSRWLNDPAFVRAQLIPDSSERNDDLY 245  
 242 YFFREDNPKNPEAPLN---SVRAOLCRGQGGESSLSVSKMNTFLKAMLYCS--DAA 295  
 246 FFFRE---KSADAPLSGVYSRIGRICLNDGGHCL-VKNKSTFLKARLVCSVPBGD 300  
 296 TNKNFNRLQDVFLPDPGQMRDTR--VGVFS--NPNMYSAVCYVSLGIDIKVFRT- 348  
 301 IETHFDELQDVEFI-----QOTQTKNPVIYAVFASGVSFGSAVCYVSMADIRVFNRP 355  
 349 -SSLKG-----YHSLPNRPGKC-----LPDQPIPTETFOVADNRHPEVAORVE 392  
 356 FAHKEGPNYQMPRTGKMPYRPETCGFTPMSKSTKDYDDEVINEMSRHATYNAVY 415  
 393 PMGPKTPPLF--HSKYHYQKVAHYRMQASGEFHYLYLTDTGTHIKV--VEEGEOHS 448  
 416 PAH--RQPLVRYTVNTRFTTIAVDQYDAADR-YEVLFTGTDGTYQKYLVLPRDMET 472  
 449 FAFNIMEIOFRRRAAIQYMSLDAERRKLVSSOWEVSQVPLDCEYVGGGCHGLMSRD 508  
 473 EELMLEIEVEKVPAPLIKMMTSSKQQLYSSAVGTALHRCQVYGEACADCCCLARD 532  
 509 PYCGMDGRCISYSS--ERSVLOSINPAEPHKECP--NPKPKAPLQKYSL-APNSRY 562  
 533 PYCAMD-GKACSRYSSASSKRSRRQDVHGNPMQCRGYNANKNVTEAVOYVEGSTA 591  
 563 YLSCPMESRHATYSW-RHKEVNEOSCEPHOSPNCI-----LFIENLTAQOYGHYCEAO 616  
 592 FLECPSPQATVYKWLQKNSDRRKELRTEGGRALRTDGLLRALQSDSGLYSTAT 651



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OY 500 CHGLMSDIPGCGDQDGRCSISTY-----SSPRVSLQSDINPAERHKECPNPK--PDKAPIQ 552
Db 526 CADCCILADPFLCANDGDISCSYTYTGTGAHAKRRFRQDVRRGNAAQOCFGQAFGDALDRT 585
OY 553 KVSIA---PNSRYVSLSCPMESRHATYSW-----RIKENVEO-----SCSPHQSPNCI 597
Db 586 EERLATGATIESNSTLLECTPRSLAQKVIWFOKGDVAKKEEVTKDDRVVKKMDLG-----L 639
OY 598 LFIENTLTAQOYTGHTFCFCAQESY 620
Db 640 LFL-RVRSKSDAGTYECQTVHEHF 661

RESULT 9
OY 9NS98 PRELIMINARY; PRT; 782 AA.
AC 09NS98; 09H703;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Semaphorin sem2 (FLJ00014 protein).
GN SEM2 OR FLJ00014.
OC (Homo sapiens (Human)).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Miyajima N.
RT Saito T.;
RL "Human semaphorin.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE OF 58-782 FROM N.A.
RC TISSUE=SPLEEN;
RA Ohara O., Nagase T., Kikuno R., Okumura K.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029496; BA098132.1; -
DR EMBL; AK024425; BAB15713.1; -
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR001627; Sema.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00423; PST; 1.
DR SMART; 782 AA; 86700 MW; 85C8424874DF6663 CR664;

Query Match 14.8%; Score 534; Db 4; Length 782;
Best Local Similarity 27.4%; Pred. No. 2, 2e-36;
Matches 194; Conservative 93; Mismatches 260; Indels 162; Gaps

OY 4 PPRGRAPASARAVPPPPARLGIPLRLRLLLIMAAASA-----QGHRSGPRFFAW 58
Db 24 PSPG---PSVRLR-----LSYRLD---SANRSATILFGQGSINTLQAMYLDEY 66
OY 59 KGHV---GOD-----RYDFQGETPHVYL-F-HEPGSSSSVWVGGRKYVLFDFEPGKNASVR 109
Db 67 RDRLEFLGDLALYSLTRDQAMPDRREVILMPRGQ----- 101
OY 110 TVNIGSTGSLDX-----RDCENYITLLERSE-GLLACGTNARHPSCWNLVNGTVPL 163
Db 102 -----REECVRRKGRDPLTECAFFAVLQPHNRTILLACGTGAFOPTCALI---TVGHR 151
OY 164 GEM-----RGYAPSPSPENSLVLFEGDEVYSTIRKEQYNGKIPRFRINGESE 211
Db 152 GEHVLHLEPGSVESGRCRPEBRRPASTFIDGELYTGL-TVDYDFGREAMIFRSGGPR 210

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QY      212 LYTSD-----TWNQNPFIKATIVHOQAVD-KIYYEFREDNDKMPKAPLN---VSRAQ 264
           |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      211 ALRSDSDSLDHPFFVMAARIPERISDNDNVFFESFVV--SPDGSNNVYTSRGR 268
QY      265 LCRDGDGSESSLSKRMVTKFLKAMLVCS---DAATKNKNRLOQVFLPDPGQWRDTRV 321
           |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      269 VCVNDAGGQGVRL-VKMWSTFLKARLVCSVPGGGAETHDDQLEDVFLMPKAG--KSLEV 325
QY      322 YGVSN---PNNYSAVCYSLGDDIKVR-----TSLKGYHSSLPNRPCKLCPD 369
           |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      326 YALFSTVASVAFGVAVCYHMADIVEVNGPRANRDRDQHWGPRVCGKVPFRPGVC-PS 384
QY      370 Q---QP-----IPETFOVARNHEVQARVERMGP---LKTPLFHSXYHQKVV 413
Db      385 KMTAPGPRFGSTKDYPRDEVLOFAANRLMTPRVPRHGRPLVLT---HLAQOLHQIV 441
QY      414 HRMQASHGETFHVLYLTTRDGRTHKV--EPGEDESHFAFNIMETIOPRRAAATQMSLD 471
           |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      442 DREAEDEG-TYDVIRPLGDSGSLVKVIALQAGSAEPREVELELOVFKVPRTIEMETS 500
QY      472 AERRLVYSSOMEVSYQVLDLCEVYGGGCHGSLMRDPYCGMDQGRCSITYSS---ERSV 528
           |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      501 VKRQLVYSGRIGVAQLRLHOCETGTCAECCLARDPACADGASCHYRSLGKRPR 560
QY      529 LOSIPAPRHEKCEPRPKDKAPLQVSL-----ANSRYYLSCPMESRHATYSWRHKEV 583
Db      561 RODIRHGNPRLALQCGSQSDEEAVGLVATMYGTENHSFLEELKRSQDAARVLLQ---- 617
QY      584 EOSCEPQHOSPNCTI-----LFENTLTAQYGHYFCEAEGSY 620
           |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      618 ----RPGEDEPQVYKTDERVLHTEKGLLFRLSRFDAGTYTCTLEHGF 662

RESULT 10
ID      08WUA9      PRELIMINARY;      PRT:      761 AA.
AC      08WUA9;
DT      01-MAR-2002 (Tremblrel, 20, created)
DT      01-MAR-2002 (Tremblrel, 20, last sequence update)
DT      01-JUN-2002 (Tremblrel, 21, last annotation update)
DE      Hypothetical 83.6 kDa protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID:9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Strausberg R.;
RA      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL      EMBL: BC020974; AAB20974.1; -
DR      InterPro: IPR000005; HTHATAC.
DR      InterPro: IPR003659; Plexin-like.
DR      InterPro: IPR002165; Plexin_repeat.
DR      InterPro: IPR001627; Sema.
DR      Pfam: PF01437; PSI; 1.
DR      Pfam: PF01403; Sema; 1.
DR      SMART: SM00423; PST; 1.
DR      PROSITE: PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
KW      Hypothetical protein.
SQ      SEQUENCE 761 AA; 83573 MW; 5BCB889AA32A2B3 CRC64;

Query Match      14.3%: Score 516; DB 4: Length 761;
Best Local Similarity 27.2%: Pred. No. 7e-35;
Matches 204; Conservative 97; Mismatches 280; Indels 168; Gaps 36.
QY      21 PPARGLPL--RLRLILLMAAASAOCHLSGPRIFVWMKNGQDRVFGOTEPHYVL 78
           |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      10 PWSLGLGLFPLDQLDLTLTTAGGGCGQPM--PRV-----RYADDERALLS-----F 55
QY      79 FHEPG-----SSVWVGGRGVYLFDF-----PECKN-----ASYRTVNIIGST 116
           |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Db 56 FHOKGLQDEDTLLSGDNTLYVGAREAILALDIDDPGVRLKNIIMPWASDR-----K 109  
 QY 117 KSCSLDKR-----DCENYI-TLLERSSEGLACGTNARHPSCH--NLVNGTVVPLG----- 164  
 Db 110 KSECAFKKSNSTOCNFRVLAVSYVTHLYCGTAFSPACFTLELOSYLEPISDEKY 169  
 QY 165 -EMRGAPRSP--DENSLVFEEDVYSTIRKOEYNGKIPREFRIRGESELEYTSDTYMOMP 222  
 Db 170 MEGKGGSPDPRAKHHTAVLDGMLYSGTW--NNFLGSEPLMKTLG-----SQPLKTD 221  
 QY 223 QFIKATIVHODAY-----DDKIYFFREDNDKKNPEAPLVNSRYAQLCRGDGGESSL 276  
 Db 222 NPLR--WLHHDASFYVAIPSTGYVYFFFEETASEDFPERLHTSRVAVRCKNDVGGKILL 279  
 QY 277 SVSKNMTFLKAMVCSDAATNKNFNRLQDVFLLPDPGSGWRDTRVYGVSPNPNY----- 331  
 Db 280 Q-KKWTTFELKAOCLLCOPG-QLEPENVIRHVVLLPADSP--TAPHIYAVETSOMQVGGTNS 335  
 QY 332 SAVCVYSLGIDDKVFR-----TSSLKGYHSSLNPNRPGKC----- 366  
 Db 336 SAVCAFSLLDIERVFGKTKELNKETSRMTTYRGPETNRPSCSGVSPSSDKALTYMKDH 395  
 QY 367 -LPDOPIPTETFOVADRHEVAQRYEPMGRLKTPLEHSHKYHOKVAVHMQASHGETH 425  
 Db 396 FLMDEQVVGTF-----PL--LVKSGVEYTRLAVETAQGLDGHSHL 432  
 QY 426 VYLITPDRGTIRKVGPEGEHSAFNIMEIOPFRRAAIIQMSLDAERKLYLVSSQWEY 485  
 Db 433 VMLGTTTSLHKAAYSGD--SSAHVLEIOLPEPDEPRVRLQLAPTOGAVFVGFSGG 489  
 QY 486 SQVPLDLCVYGGCHGCLMSRDPYCGMD-QGR--CISYSSERYSLQGINPAEPHKECP 542  
 Db 490 WNVPRANCYV--ESCVDYCLARPHCAMPEBSRTCCLLSAPNINSMKODMERENPBMACA 548  
 QY 543 NP-----KPKAP--LQVYSLAPNSRYLSCPMESRHATYSRKHEKNVQSCERPQSD 594  
 Db 549 SCPMSRSLRPOSROPILIKIEVLAVPNSILPECPHLSALASYWSHGPAVPEASSTVYNG 608  
 QY 595 NCILFENTTAQOYGHYFCEAOEG-----SYFREAOHMLL--PE-DGIMAEHL-- 641  
 Db 609 SLILYQDVG--GLYQCMATENGFSYVITWYDSDOTLALDELAGIPIREHKVPL 665  
 QY 642 -----GHACALASLWLGVLPTLLGLLV 665  
 Db 666 TRVSGAALAAQSYWPHFVTYVLEALV 694

RESULT 11  
 Q9C0C4 PRELIMINARY; PRT: 963 AA.  
 ID Q9C0C4  
 AC Q9C0C4  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE KIAI1739 protein (Fragment).  
 GN KIAI1739.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082932; PubMed=11214970;  
 RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XIX.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 7:347-355(2000).  
 DR EMBL; AB051526; BAB21830.1; -  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003600; Ig\_like.  
 DR InterPro; IPR003659; Plexin-like.  
 DR InterPro; IPR002165; Plexin\_repeat.

DR InterPro; IPR001627; Sema.  
 DR Pfam; PF01437; PSI; 1.  
 DR SMART; SM00403; Sema; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00410; IG\_like; 1.  
 DR SMART; SM00423; PSI; 1.  
 DR NON\_TER  
 SQ SEQUENCE 963 AA; 106735 MW; 3FA37DBBA3483ECE CRC64;  
 Query Match 13.8%; Score 500.5; DB 4; Length 963;  
 Best Local Similarity 26.4%; Pred. No. 2e-33;  
 Matches 181; Conservative 100; Mismatches 268; Indels 137; Gaps 34;  
 QY 64 QDRVDFGQEPHNTVLFHEPSSSVWVGGRKYYLFPPEBKNSVKTVINGST----- 116  
 Db 181 QDFLTLLTPEPTGLY-----VGARALFAF-----SMEALEQGAISWEAPV 223  
 QY 117 --KSCSLDK-----RCENYITLLE--RSEGLACGTNARHPSCHMLVNGTVVPL--GEM 166  
 Db 224 EKTETCIQKKNQGTGCFNFRFLQRYNASHLYVCGTYAFQPKC--TYVNMILFTLEHGEF 282  
 QY 167 ---RGYAPSPDENSLVFEEDVYSTIRKOEYNGKIPREFRIRGESELEYTSDTV---MQ 220  
 Db 283 EDEKKGCPYDPAKGAGLVDGELYSA--TLNPLGTEPILIRMMGPHNSKTEYLAFWLN 341  
 QY 221 NPOFIKATIVHOD-----QAVDDKIYFFREDNDKKNPEAPLVNSRYAQLCRGDGGESSL 276  
 Db 342 EPHFVGSATVPESVSGFTGDDKVYFFERAVESDCAQVAVARAVCKGDMGARLT 401  
 QY 277 SVSKNMTFLKAMVCSDAATNKNFNRLQDVFLLPDPGSGWRDTRVYGVSPNPNY-----YSA 333  
 Db 402 Q-KKWTTFELKARLACAPNMQLFENQLOAMHTLQDTS--WHNTPFGVFOAGMDYLSA 458  
 QY 334 VCYSISGDDIDKVRTSLSKYHSS-----LPNPRGKCL-----PDQPIR 374  
 Db 459 ICEYOLEEIORVPE--GPYKEYHEAQKWDRTYDVPSPRGSCINMHRHNGYTSLELP 517  
 QY 375 TETFOVADRHEVAQRYEPMGRLKTPLEHSHKYHOKVAVHMQASHGETHLYTTDR 433  
 Db 518 DNILNVKKIPLLEBOGPR--WSRPLVKKGTNFTHLVADRGTGLDGAITYLVLTGTGD 575  
 QY 434 GTIRKVGPEGEHSAFNIMEIOPFRRAAIIQMSLDAERKLYLVSSQWEVSQLPDL 493  
 Db 576 GWLKAIVSLGPVWHL-----IEELQFLDQ--EPMKSLVLSQSKLLPFGSRQLDLPVADC 630  
 QY 494 EYVGGCGHCLMSRDPYCGM--DQGRCSITYSSERYL-QSINPAEPHKEC----- 541  
 Db 631 MKY-RSCADCVLARDPYCAWSVNTSRCAVAGHSGSLILOHVMTPDSGICNLRSKVR 689  
 QY 542 PNPKPAPLQKYSLAPNSRYLSCPMESR--HATYSMRKHEKNVQSCERPQSD 599  
 Db 690 PTKR-----NITVAAGTDLVLPCHLSSNLAMARKTFGGRD-----LPAEQ-PSGFY 735  
 QY 600 IENULTA-----QOYGHYFCEAOEGSYFREAOHMLLPEDSIMAEHLGHACALAS- 650  
 Db 736 DARLQALVWMAQPRHAGAVHC-----FSEQGARLAIE-GYLAVVAVGSPVSTLEARA 767  
 QY 651 -----LNLGVLP-----TLTGLLV 665  
 Db 788 PLENLGLWLVAVLGAVALCLVLLLV 813

RESULT 12  
 Q9P2H9 PRELIMINARY; PRT: 1049 AA.  
 ID Q9P2H9  
 AC Q9P2H9  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE KIAI1368 protein (Fragment).  
 GN KIAI1368.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRIN:  
RX MEDLINE=2018126; PubMed=10718198;  
RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XVI.  
RT The complete sequences of 150 new cDNA clones from brain which code  
RT for large proteins in vitro."  
RL DNA Res. 7:65-73(2000).  
DR EMBL: AB037789; BA92606.1;  
DR InterPro: IPR003659; Plexin-like.  
DR InterPro: IPR001627; Sema.  
DR Pfam: PF01403; Sema; 1.  
DR SMART: SM00423; PSI; 1.  
DR NON\_TER 1  
SQ SEQUENCE 1049 AA; 116511 MW; 7781D20AC7A8A6A CRC64;  
  
Query Match 12.3%; Score 444.5; DB 4; Length 1049;  
Best Local Similarity 26.5%; Pred. No. 1.3e-28;  
Matches 162; Conservative 78; Mismatches 251; Indels 120; Gaps 27;  
  
DB 80 HEPG-----SSSVWGGRGVYLFDEPEEGKNASV-----RTVN 112  
46 HKPGNTQRRHLDIOMIMNGTLYIAROHIVYDIDTSHTEELYSCKLTKWRSROAD 105  
113 IGSTGSCIDKRCENYI-TLLERSEGLACGTNARHPSCNLVNGTVPLG-EMRGYA 170  
106 VDTCKMKRKHKECHNFVKLLKNDALFYCGTNAFNSCNYMDTLEPGDEFGMA 165  
171 --PSPDENSIVLFEEDVYS-----TIKQEVN--GKIPRRIRGESELYSDTYM 219  
166 RCPYAKAHANVALFADGKLYSATVDTFLAIDAVIYRSLGESPTLRTVKHDSKW-----L 219  
220 QNPQIKATYIHOQAYDDKIYFFREDNPKNPAPLNVSAVALCRDGGESSLSYS 279  
220 KEPEFVQAV-----DYGDIYFFREIAYEVNTMGKVFPPVAQVCKNDMGSGRVLEK 273  
280 KWNFLKAMLYCS-DAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPNVY---SAVC 335  
274 QWTSFLKARLNCVSGDHSFYFNILQAVTVIRING--RDV-VLATFTSPYNSIPGSAVC 330  
336 VYSLGDDIKVFTSSLKGYHS-----SLPNPRGKC-----LPDQPIFTE 376  
331 AYDMLDIASVF-TGRFKKOKSPDSTWTPVDERVYKPRPGCCAGSSSLERYATSNEFPD 389  
377 TFOVADRHREVAQRYEPMPGLKTPLE---HSKYHYQKVAVHRMQASHGETFHVLYLTDR 433  
390 TLNFKTHPLMDQAVPSI--FNRPWFELRTWRYRLTKLTAIVDTAAGPY-QNHTVVLGSEK 446  
434 GTIHK-----VEPEGOEHSFAFNIMEIOFPRRAA-----AIQTMSLDAERKLYVSQ 482  
447 GILKFLARINSGFLNLSLFLSEMSVYNSEKCSYDVEDKRIMQMOLDRASSSLTYAFS 506  
483 WEVSQVPLDCEVYGGGCHGLMSRDPYCGM--DQGRCSISYSSRSVL-OSINAEPH- 538  
507 TCVIVKPLRGCEBHKCKKCTIASRDPYCGMIKEGACSHLSPNRLTFEODIERGNTDG 566  
539 -KECPN-----PKPDKAPLOKV-----SLAPNSRYLLSCP--ESRHAITYSMR 578  
567 LGDCHNSVALNDISTPLPDNEMSTNYVYGHSSSLPSTTTSDSTAQEGYESRGMIDWK 626  
627 HLDSPTDTP 637  
  
RESULT 13  
ID 09H2E6 PRELIMINARY; PRT: 1030 AA.  
AC 09H2E6;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Semaphorin SEMA6A1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20564339; PubMed=10993894;  
RA Klosternann A., Lutz B., Gertler F., Behl C.;  
RT "The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-  
RT 1/SEMA6A-1) bind to the Enabled/Vasodilator-stimulated Phosphoprotein-  
RT like Protein (EVL) via a novel carboxyl-terminal Zyxin-like domain."  
RL J. Biol. Chem. 275:39647-39653(2000).  
DR EMBL: AF279656; AAC29378.1;  
DR InterPro: IPR003659; Plexin-like.  
DR InterPro: IPR001627; Sema.  
DR Pfam: PF01403; Sema; 1.  
DR SMART: SM00423; PSI; 1.  
SQ SEQUENCE 1030 AA; 114368 MW; A57B79C10AEC4B34 CRC64;  
  
Query Match 12.1%; Score 437; DB 4; Length 1030;  
Best Local Similarity 26.1%; Pred. No. 5.4e-28;  
Matches 161; Conservative 80; Mismatches 251; Indels 126; Gaps 27;  
  
DB 80 HEPG-----SSSVWGGRGVYLFDEPEEGKNASV-----RTVN 112  
44 HKPGNTQRRHLDIOMIMNGTLYIAROHIVYDIDTSHTEELYSCKLTKWRSROAD 103  
113 IGSTGSCIDKRCENYI-TLLERSEGLACGTNARHPSCNLVNGTVPLG-EMRGYA 170  
104 VDTCKMKRKHKECHNFVKLLKNDALFYCGTNAFNSCNYMDTLEPGDEFGMA 163  
171 --PSPDENSIVLFEEDVYS-----TIKQEVN--GKIPRRIRGESELYSDTYM 219  
164 RCPYAKAHANVALFADGKLYSATVDTFLAIDAVIYRSLGESPTLRTVKHDSKW-----L 217  
220 QNPQIKATYIHOQAYDDKIYFFREDNPKNPAPLNVSAVALCRDGGESSLSYS 279  
218 KEPEFVQAV-----DYGDIYFFREIAYEVNTMGKVFPPVAQVCKNDMGSGRVLEK 271  
280 KWNFLKAMLYCS-DAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPNVY---SAVC 335  
272 QWTSFLKARLNCVSGDHSFYFNILQAVTVIRING--RDV-VLATFTSPYNSIPGSAVC 328  
336 VYSLGDDIKVFTSSLKGYHS-----SLPNPRGKC-----LPDQPIFTE 376  
329 AYDMLDIASVF-TGRFKKOKSPDSTWTPVDERVYKPRPGCCAGSSSLERYATSNEFPD 387  
377 TFOVADRHREVAQRYEPMPGLKTPLE---HSKYHYQKVAVHRMQASHGETFHVLYLTDR 433  
388 TLNFKTHPLMDQAVPSI--FNRPWFELRTWRYRLTKLTAIVDTAAGPY-QNHTVVLGSEK 444  
434 GTIHK-----VEPEGOEHSFAFNIMEIOFPRRAA-----AIQTMSLDAERKLYVSQ 482  
445 GILKFLARINSGFLNLSLFLSEMSVYNSEKCSYDVEDKRIMQMOLDRASSSLTYAFS 504  
483 WEVSQVPLDCEVYGGGCHGLMSRDPYCGM--DQGRCSISYSSRSVL-OSINAEPH- 538  
505 TCVIVKPLRGCEBHKCKKCTIASRDPYCGMIKEGACSHLSPNRLTFEODIERGNTDG 564  
539 -KECPN-----PKPDKAPLOKV-----SLAPNSRYLLSCP--ESRHAITYSMR 578  
565 LGDCHN-----SFVALNGHSSSLPSTTTSDSTAQEGYESRGMIDWKHLDSPTD 616  
588 EP-----GHOSPNCIL 598  
617 DPLGAVSSHNHQQDKGVI 634  
  
RESULT 14  
ID 09J129



us-09-836-077-3.rsp

RL	DNA	Query Best I Matches
DR	EME	QY 5
DR	Int	QY 6
DR	Int	Db 15
DR	Int	QY 11
DR	Int	Db 21
DR	Int	QY 16
DR	Int	Db 27
DR	Int	QY 21
DR	Int	Db 33
DR	Int	QY 27
DR	Int	Db 37
DR	Int	QY 33
DR	Int	Db 43
DR	Int	QY 47
DR	Int	Db 53
DR	Int	QY 48
DR	Int	Db 60
DR	Int	QY 53
DR	Int	Db 66
DR	Int	QY 57
DR	Int	Db 73

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